

SEQUENCE LISTING

<110> Croteau, Rodney B  
Bohlmann, Joerg  
Steele, Christopher L  
Phillips, Michael A

<120> MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

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<150> 09/360,545  
<151> 1999-07-26

<150> 60/052,249  
<151> 1997-07-11

<150> PCT/US98/14528  
<151> 1998-07-10

<160> 107

<170> PatentIn Ver. 2.0

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<223> Clone AG2.2 encoding myrcene synthase

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Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys  
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ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158  
Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr  
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aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206  
Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr  
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cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254  
Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val  
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Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe  
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Leu	Asp	Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	
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Leu	Trp	Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	
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Lys	Asn	Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	
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Ser	Thr	Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	
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Tyr	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	
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Ala	Glu	Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	
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Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	
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Leu	Glu	Lys	Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	
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ttc gcc aaa atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac Phe Ala Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp 370 375 380			1214
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aga tgg aat tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt Arg Trp Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys 400 405 410			1310
gtg tac atg gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg Val Tyr Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala 415 420 425 430			1358
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tat atg aaa gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat Tyr Met Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His 545 550 555			1742
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575 580 585 590

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Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu  
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Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile  
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Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val  
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His Lys Ser Leu Ile Ser Ser Thr His Glu Leu Lys Ala Leu Ser Arg  
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Thr Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro  
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Ser Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg  
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Arg Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile  
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Asp Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu  
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290 295 300

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Pro Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu  
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580 585 590

gac atc gcc aga gct ttc cat tac ggc tac aaa tac cga gac ggc tac 1826  
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Glu Ser Val Pro Leu  
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Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile Gln  
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Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala Glu  
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Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu Glu  
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Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu Trp  
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Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys Asp  
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Glu Ile Phe Ser Thr Lys Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro		
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Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly Trp		
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His Thr Tyr Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Gln Val Phe		
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Gly Gln Asp Thr Glu Asn Thr Lys Ser Tyr Val Lys Ser Lys Lys Leu		
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Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly Phe		
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Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile  
545 550 555 560

Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu Leu  
565 570 575

Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp  
580 585 590

Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr Ser  
595 600 605

Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu Glu  
610 615 620

Ser Val Pro Leu  
625

<210> 5

<211> 2089

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (73)..(1986)

<223> Clone AG10 encoding limonene synthase

<400> 5

tgccgtttaa tcgggttaaa gaagctacca tagtcgggt taaagaagct accatagtt 60

aggcaggaat cc atg gct ctc ctt tct atc gta tct ttg cag gtt ccc aaa 111  
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys  
1 5 10

tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159  
Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Asn Val Gln Lys Ala  
15 20 25

ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207  
Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln  
30 35 40 45

aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255  
Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp  
50 55 60

gat aat ggt ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303  
Asp Asn Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro  
65 70 75

aac ctg tgg gaa gat gat ttc ata caa tca ttg tcc tca cct tat ggg 351  
Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly  
80 85 90

gga tct tcg tac agt gaa cgt gct gag aca gtc gtt gag gaa gta aaa 399  
Gly Ser Ser Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys  
95 100 105

gag atg ttc aat tca ata cca aat aat aga gaa tta ttt ggt tcc caa 447  
Glu Met Phe Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln  
110 115 120 125

aat gat ctc ctt aca cgc ctt tgg atg gtg gat agc att gaa cgt ctg 495  
Asn Asp Leu Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu  
130 135 140

ggg ata gat aga cat ttc caa aat gag ata aga gta gcc ctc gat tat 543  
Gly Ile Asp Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr  
145 150 155

gtt tac agt tat tgg aag gaa aag gaa ggc att ggg tgt ggc aga gat 591  
Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp  
160 165 170

tct act ttt cct gat ctc aac tcg act gcc ttg gcg ctt cga act ctt 639  
Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu  
175 180 185

cga ctg cac gga tac aat gtg tct tca gat gtg ctg gaa tac ttc aaa 687  
Arg Leu His Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys  
190 195 200 205

gat gaa aag ggg cat ttt gcc tgc cct gca atc cta acc gag gga cag 735  
Asp Glu Lys Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln  
210 215 220

atc act aga agt gtt cta aat tta tat cgg gct tcc ctg gtc gcc ttt 783  
Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe  
225 230 235

ccc ggg gag aaa gtt atg gaa gag gct gaa atc ttc tcg gca tct tat 831  
Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr  
240 245 250

ttg aaa aaa gtc tta caa aag att ccg gtc tcc aat ctt tca gga gag 879  
Leu Lys Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu  
255 260 265

ata gaa tat gtt ttg gaa tat ggt tgg cac acg aat ttg ccg aga ttg 927  
Ile Glu Tyr Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu  
270 275 280 285

gaa gca aga aat tat atc gag gtc tac gag cag acg ggc tat gaa agc 975  
Glu Ala Arg Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser  
290 295 300

tta aac gag atg cca tat atg aac atg aag aag ctt tta caa ctt gca 1023  
Leu Asn Glu Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala  
305 310 315

aaa ttg gag ttc aat atc ttt cac tct ttg caa cta aga gag tta caa Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln 320 325 330	1071
tct atc tcc aga tgg tgg aaa gaa tca ggt tcg tct caa ctg act ttt Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe 335 340 345	1119
aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser 350 355 360 365	1167
atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys 370 375 380	1215
cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met 385 390 395	1263
aac gaa ctc caa ctt ttt acg gat gca att aag aga tgg gat ttg tca Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser 400 405 410	1311
acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu 415 420 425	1359
tat caa tgc att aat gaa atg gtg gaa gag gct gag aag act caa ggc Tyr Gln Cys Ile Asn Glu Met Val Glu Ala Glu Lys Thr Gln Gly 430 435 440 445	1407
cga gat atg ctc aac tat att caa aat gct tgg gaa gcc cta ttt gat Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp 450 455 460	1455
acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Tyr Leu Pro Thr 465 470 475	1503
ttt gag gag tac ttg aag aat gca aaa gtt agt tct ggt tct cgc ata Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile 480 485 490	1551
gcc aca tta caa ccc att ctc act ttg gat gta cca ctt cct gat tac Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr 495 500 505	1599
ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcg Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser 510 515 520 525	1647
tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg 530 535 540	1695
gcc cgt gga gaa gaa gct tca gct ata tcg tgt tat atg aaa gac cat Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His 545 550 555	1743
cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc	1791

Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile  
560 565 570

agt gat gca atc aga gaa tta aat tgg gag ctt ctc aga ccg gat agc 1839  
Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser  
575 580 585

aaa agt ccc atc tct tcc aag aaa cat gct ttt gac atc acc aga gct 1887  
Lys Ser Pro Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala  
590 595 600 605

ttc cat cat gtc tac aaa tat cga gat ggt tac act gtt tcc aac aac 1935  
Phe His His Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn  
610 615 620

gaa aca aag aat ttg gtg atg aaa acc gtt ctt gaa cct ctc gct ttg 1983  
Glu Thr Lys Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu  
625 630 635

taa aaacatataag aatgcattaa aatgtggaa gtctataatc tagactattc 2036

tctatcttc ataatgtaga tctggatgtg tattgaactc taaaaaaaaaaa aaa 2089

<210> 6  
<211> 637  
<212> PRT  
<213> Abies grandis

<400> 6  
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly  
1 5 10 15

Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile  
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu  
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly  
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp  
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser  
85 90 95

Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe  
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu  
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp  
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser  
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe  
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His  
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Glu Lys  
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg  
210 215 220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu  
225 230 235 240

Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Lys  
245 250 255

Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu Ile Glu Tyr  
260 265 270

Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg  
275 280 285

Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser Leu Asn Glu  
290 295 300

Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala Lys Leu Glu  
305 310 315 320

Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln Ser Ile Ser  
325 330 335

Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe Thr Arg His  
340 345 350

Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Leu Pro  
355 360 365

Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys His Leu Val  
370 375 380

Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asn Glu Leu  
385 390 395 400

Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser Thr Thr Arg  
405 410 415

Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu Tyr Gln Cys  
420 425 430

Ile Asn Glu Met Val Glu Ala Glu Lys Thr Gln Gly Arg Asp Met  
435 440 445

Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp Thr Phe Met  
450 455 460

Gln Glu Ala Lys Trp Ile Ser Ser Tyr Leu Pro Thr Phe Glu Glu  
465 470 475 480

Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile Ala Thr Leu

485

490

495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr Ile Leu Gln  
500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser Ser Ile Leu  
515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly  
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser  
545 550 555 560

Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Ser Asp Ala  
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro  
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His  
595 600 605

Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn Glu Thr Lys  
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu  
625 630 635

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Degenerate  
oligonucleotide PCR primer A wherein the letter  
"n" indicates an inosine residue

<220>

<221> misc\_feature

<222> (1)..(25)

<223> Degenerate oligonucleotide Primer A wherein n  
represents inosine

<400> 7

arraygarra nggnrartay aarga

25

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate  
oligonucleotide PCR primer B wherein the letter  
"n" represents an inosine residue

<220>

<221> misc\_feature  
<222> (1)..(20)  
<223> oligonucleotide PCR primer B wherein the letter n  
represents an inosine residue

<400> 8  
atgytncary tntaygargc

20

<210> 9  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: degenerate  
oligonucleotide PCR primer C wherein the letter  
"n" represents an inosine residue

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223> PCR primer C wherein the letter n represents  
inosine

<400> 9  
ctnkynrang gncatratrta cktv

24

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: degenerate  
oligonucleotide PCR primer D wherein the letter  
"n" represents an inosine residue

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223> PCR primer D wherein the letter n represents  
inosine

<400> 10  
gaygaynnnt wygaygcnya ygg

23

<210> 11  
<211> 108  
<212> DNA  
<213> Artificial Sequence

<400> 11  
gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60  
agaagatggg acctctcctt tacagacaac ttcccccatt acatgaaa

108

<210> 12

<211> 104

<212> DNA

<213> Abies grandis

<400> 12

gacgacgggt atgatgcgca tggaacgatt gacgagctt aactcttcac atctgcaatt 60

aagagatgga attcatcaga gatagacagc ttcccccact atat

104

<210> 13

<211> 105

<212> DNA

<213> Abies grandis

<220>

<221> misc\_feature

<222> (89)

<223> nucleotide may be a or c or g or t

<400> 13

gatgatgggt atgatgcgta cggaacgttg gaagaatca aaatcatgac agagggagtg 60

agacgatggg atcttcgtt gaccgcttnc cccgactata tgaaa

105

<210> 14

<211> 117

<212> DNA

<213> Abies grandis

<220>

<221> misc\_feature

<222> (93)

<223> nucleotide may be a or c or g or t

<400> 14

gacgatgggt atgatgcgca tggaaccttg gaccaactca aaatcttac agagggagtg 60

agacgatggg atgtttcggtt ggttagaccac ttnccccac tacatgcaat ctagacc 117

<210> 15

<211> 2424

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (2)..(2350)

<223> Clone AG1.28

<400> 15

g ggt tat gat ctt gtg cat tct ctt aaa tca cct tat att gat tct agt 49  
Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser

1

5

10

15

tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97  
Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu

20

25

30

aat cca gct att aca gga gat gga gaa tca atg att act cca tct gct 145  
Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala  
35 40 45

tat gac aca gca tgg gta gcg agg gtg ccc gcc att gat ggc tct gct 193  
Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala  
50 55 60

cgc ccg caa ttt ccc caa aca gtt gac tgg att ttg aaa aac cag tta 241  
Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu  
65 70 75 80

aaa gat ggt tca tgg gga att cag tcc cac ttt ctg ctg tcc gac cgt 289  
Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg  
85 90 95

ctt ctt gcc act ctt tct tgt gtt ctt gtg ctc ctt aaa tgg aac gtt 337  
Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Lys Trp Asn Val  
100 105 110

ggg gat ctg caa gta gag cag gga att gaa ttc ata aag agc aat ctg 385  
Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu  
115 120 125

gaa cta gta aag gat gaa acc gat caa gat agc ttg gta aca gac ttt 433  
Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe  
130 135 140

gag atc ata ttt cct tct ctg tta aga gaa gct caa tct ctg cgc ctc 481  
Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu  
145 150 155 160

gga ctt ccc tac gac ctg cct tat ata cat ctg ttg cag act aaa cgg 529  
Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg  
165 170 175

cag gaa aga tta gca aaa ctt tca agg gag gaa att tat gcg gtt ccg 577  
Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro  
180 185 190

tcg cca ttg ttg tat tct tta gag gga ata caa gat ata gtt gaa tgg 625  
Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp  
195 200 205

gaa cga ata atg gaa gtt caa agt cag gat ggg tct ttc tta agc tca 673  
Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser  
210 215 220

cct gct tct act gcc tgc gtt ttc atg cac aca gga gac gcg aaa tgc 721  
Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys  
225 230 235 240

ctt gaa ttc ttg aac agt gtg atg atc aag ttt gga aat ttt gtt ccc 769  
Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro  
245 250 255

tgc ctg tat cct gtg gat ctg ctg gaa cgc ctg ttg atc gta gat aat 817  
Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn  
260 265 270

att gta cgc ctt gga atc tat aga cac ttt gaa aag gaa atc aag gaa 865

Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu  
275 280 285

gct ctt gat tat gtt tac agg cat tgg aac gaa aga gga att ggg tgg 913  
Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp  
290 295 300

ggc aga cta aat ccc ata gca gat ctt gag acc act gct ttg gga ttt 961  
Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe  
305 310 315 320

cga ttg ctt cgg ctg cat agg tac aat gta tct cca gcc att ttt gac 1009  
Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp  
325 330 335

aac ttc aaa gat gcc aat ggg aaa ttc att tgc tcg acc ggt caa ttc 1057  
Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe  
340 345 350

aac aaa gat gta gca agc atg ctg aat ctt tat aga gct tcc cag ctc 1105  
Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu  
355 360 365

gca ttt ccc gga gaa aac att ctt gat gaa gct aaa agc ttc gct act 1153  
Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr  
370 375 380

aaa tat ttg aga gaa gct ctt gag aaa agt gag act tcc agt gca tgg 1201  
Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp  
385 390 395 400

aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act 1249  
Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr  
405 410 415

tct tgg cat gcc agt gtt ccg aga gtg gaa gca aag aga tac tgt caa 1297  
Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln  
420 425 430

gtg tat cgc cca gat tat gca cgc ata gca aaa tgc gtt tac aag cta 1345  
Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu  
435 440 445

ccc tac gtg aac aat gaa aag ttt tta gag ctg gga aaa tta gat ttc 1393  
Pro Tyr Val Asn Asn Glu Phe Leu Glu Leu Gly Lys Leu Asp Phe  
450 455 460

aac att atc cag tcc atc cac caa gaa gaa atg aag aat gtt acc agc 1441  
Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser  
465 470 475 480

tgg ttt aga gat tcg ggg ttg cca cta ttc acc ttc gct cgg gag agg 1489  
Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg  
485 490 495

ccg ctg gaa ttc tac ttc tta gta gcg gcg ggg acc tat gaa ccc cag 1537  
Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln  
500 505 510

tat gcc aaa tgc agg ttc ctc ttt aca aaa gtg gca tgc ttg cag act 1585  
Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr

515	520	525	
gtt ctg gac gat atg tat gac act tat gga acc cta gat gaa ttg aag Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys 530	535	540	1633
cta ttc act gag gct gtg aga aga tgg gac ctc tcc ttt aca gaa aac Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn 545	550	555	1681
ctt cca gac tat atg aaa cta tgt tac caa atc tat tat gac ata gtt Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val 565	570	575	1729
cac gag gtg gct tgg gag gca gag aag gaa cag ggg cgt gaa ttg gtc His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val 580	585	590	1777
agc ttt ttc aga aag gga tgg gag gat tat ctt ctg ggt tat tat gaa Ser Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu 595	600	605	1825
gaa gct gaa tgg tta gct gct gag tat gtg cct acc ttg gac gag tac Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr 610	615	620	1873
ata aag aat gga atc aca tct atc ggc caa cgt ata ctt ctg ttg agt Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Ser 625	630	635	1921
gga gtg ttg ata atg gat ggg caa ctc ctt tcg caa gag gca tta gag Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu 645	650	655	1969
aaa gta gat tat cca gga aga cgt gtt ctc aca gag ctg aat agc ctc Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu 660	665	670	2017
att tcc cgc ctg gcg gat gac acg aag aca tat aaa gct gag aag gct Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala 675	680	685	2065
cgt gga gaa ttg gcg tcc agc att gaa tgt tac atg aaa gac cat cct Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro 690	695	700	2113
gaa tgt aca gag gaa gag gct ctc gat cac atc tat agc att ctg gag Glu Cys Thr Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu 705	710	715	2161
ccg gcg gtg aag gaa ctg aca aga gag ttt ctg aag ccc gac gac gtc Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val 725	730	735	2209
cca ttc gcc tgc aag aag atg ctt ttc gag gag aca aga gtg acg atg Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met 740	745	750	2257
gtg ata ttc aag gat gga gat gga ttc ggt gtt tcc aaa tta gaa gtc Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val 755	760	765	2305

aaa gat cat atc aaa gag tgt ctc att gaa ccg ctg cca ctg taa 2350  
Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu  
770 775 780

tcaaaaatagt tgcaataata attgaaataa tgtcaactat gtttcacaaaa aaaaaaaaaa 2410  
aaaaaaaaaaa aaaa 2424

<210> 16  
<211> 782  
<212> PRT  
<213> Abies grandis

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20 25 30

Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala  
35 40 45

Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala  
50 55 60

Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu  
65 70 75 80

Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg  
85 90 95

Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Lys Trp Asn Val  
100 105 110

Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu  
115 120 125

Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe  
130 135 140

Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu  
145 150 155 160

Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg  
165 170 175

Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro  
180 185 190

Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp  
195 200 205

Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser  
210 215 220

Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys  
225 230 235 240

Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro  
245 250 255

Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn  
260 265 270

Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu  
275 280 285

Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp  
290 295 300

Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe  
305 310 315 320

Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp  
325 330 335

Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe  
340 345 350

Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu  
355 360 365

Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr  
370 375 380

Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp  
385 390 395 400

Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr  
405 410 415

Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln  
420 425 430

Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu  
435 440 445

Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe  
450 455 460

Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser  
465 470 475 480

Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg  
485 490 495

Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln  
500 505 510

Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr  
515 520 525

Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys  
530 535 540

Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn  
545 550 555 560

Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val

565

570

575

His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val  
580 585 590

Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu  
595 600 605

Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr  
610 615 620

Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser  
625 630 635 640

Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu  
645 650 655

Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu  
660 665 670

Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala  
675 680 685

Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro  
690 695 700

Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu  
705 710 715 720

Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val  
725 730 735

Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met  
740 745 750

Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val  
755 760 765

Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu  
770 775 780

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<211> 1967

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (3)..(1736)

<223> Clone AG4.30

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Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His His Gly Asn  
1 5 10 15

gtg tgg gac gat gac ctc ata cac tct ctc aac tcg ccc tat ggg gca 95  
Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala  
20 25 30

cct gca tat tat gag ctc ctt caa aag ctt att gag gag atc aag cat 143  
Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His  
35 40 45

tta ctt ttg act gaa atg gaa atg gat gat ggc gat cat gat tta atc 191  
Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile  
50 55 60

aaa cgt ctt cag atc gtt gac act ttg gaa tgc ctg gga atc gat aga 239  
Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg  
65 70 75

cat ttt gaa cac gaa ata caa aca gct gct tta gat tac gtt tac aga 287  
His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg  
80 85 90 95

tgg tgg aac gaa aaa ggt atc ggg gag gga tca aga gat tcc ttc agc 335  
Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser  
100 105 110

aaa gat ctc aac gct aca gct tta gga ttt cgc gct ctc cga ctg cat 383  
Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His  
115 120 125

cga tat aac gta tcg tca ggt gtg ttg aag aat ttc aag gat gaa aac 431  
Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn  
130 135 140

ggg aag ttc ttc tgc aac ttt act ggt gaa gaa gga aga gga gat aaa 479  
Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys  
145 150 155

caa gtg aga agc atg ttg tcg tta ctt cga gct tca gag att tcg ttt 527  
Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe  
160 165 170 175

ccc gga gaa aaa gtg atg gaa gag gcc aag gca ttc aca aga gaa tat 575  
Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr  
180 185 190

cta aac caa gtt tta gct gga cac ggg gat gtg act gac gtg gat caa 623  
Leu Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln  
195 200 205

agc ctt ttg gag aga ggt gaa gta cgc att gga gtt tcc atg gct tgc 671  
Ser Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys  
210 215 220

agt gtg ccg aga tgg gag gca agg agc ttt ctc gaa ata tat gga cac 719  
Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His  
225 230 235

aac cat tcg tgg ctc aag tcg aat atc aac caa aaa atg ttg aag tta 767  
Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu  
240 245 250 255

gcc aaa ttg gac ttc aat att ctg caa tgc aaa cat cac aag gag ata 815  
Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile  
260 265 270

cag ttt att aca agg tgg tgg aga gac tcg ggt ata tcg cag ctg aat 863

Gln Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn  
275 280 285

ttc tat cga aag cga cac gtg gaa tat tat tct tgg gtt gtt atg tgc 911  
Phe Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys  
290 295 300

att ttt gag cca gag ttc tct gaa agt aga att gcc ttc gcc aaa act 959  
Ile Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr  
305 310 315

gct atc cta tgt act gtt cta gat gac ctc tat gat acg cac gca acg 1007  
Ala Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr  
320 325 330 335

ttg cat gaa atc aaa atc atg aca gag gga gtg aga cga tgg gat ctt 1055  
Leu His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu  
340 345 350

tcg ttg aca gat gac ctc cca gac tac att aaa att gca ttc cag ttc 1103  
Ser Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe  
355 360 365

ttc ttc aat aca gtg aat gaa ttg ata gtt gaa atc gtg aaa cgg caa 1151  
Phe Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln  
370 375 380

ggg cgg gat atg aca acc ata gtt aaa gat tgc tgg aag cga tac att 1199  
Gly Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile  
385 390 395

gag tct tat ctg caa gaa gcg gaa tgg ata gca act gga cat att ccc 1247  
Glu Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro  
400 405 410 415

act ttt aac gaa tac ata aag aac ggc atg gct agc tca ggg atg tgt 1295  
Thr Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys  
420 425 430

att gta aat ttg aat cca ctt ctc ttg ttg ggt aaa ctt ctc ccc gac 1343  
Ile Val Asn Leu Asn Pro Leu Leu Leu Gly Lys Leu Leu Pro Asp  
435 440 445

aac att ctg gag caa ata cat tct cca tcc aag atc ctg gac ctc tta 1391  
Asn Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu  
450 455 460

gaa ttg acg ggc aga atc gcc gat gac tta aaa gat ttc gag gac gag 1439  
Glu Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu  
465 470 475

aag gaa cgc ggg gag atg gct tca tct tta cag tgt tat atg aaa gaa 1487  
Lys Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu  
480 485 490 495

aat cct gaa tct aca gtg gaa aat gct tta aat cac ata aaa ggc atc 1535  
Asn Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile  
500 505 510

ctt aat cgt tcc ctt gag gaa ttt aat tgg gag ttt atg aag cag gat 1583  
Leu Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp

515	520	525	
agt gtc cca atg tgt tgc aag aaa ttc act ttc aat ata ggt cga gga			1631
Ser Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly			
530	535	540	
ctt caa ttc atc tac aaa tac aga gac ggc tta tac att tct gac aag			1679
Leu Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys			
545	550	555	
gaa gta aag gac cag ata ttc aaa att cta gtc cac caa gtt cca atg			1727
Glu Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met			
560	565	570	575
gag gaa tag tgatggctt gggttagtt gtctattatg gtatattgca			1776
Glu Glu			
ttgacatata tgcttaaagg tgtttcttaa acgttaggg cggaccgtta aataagttgg			1836
caataattaa tatttagaga ctttggaa gtgttaggg cataaaaattt cctatggcct			1896
atggcaagct acaaattgaa attgttgtt ttataatatt ttatattttt ttaaaaaaaaa			1956
aaaaaaaaaa a			1967
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<212> PRT			
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Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala Pro			
20	25	30	
Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His Leu			
35	40	45	
Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile Lys			
50	55	60	
Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg His			
65	70	75	80
Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg Trp			
85	90	95	
Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser Lys			
100	105	110	
Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His Arg			
115	120	125	
Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn Gly			
130	135	140	
Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys Gln			
145	150	155	160

Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe Pro  
165 170 175

Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr Leu  
180 185 190

Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln Ser  
195 200 205

Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys Ser  
210 215 220

Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His Asn  
225 230 235 240

His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu Ala  
245 250 255

Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile Gln  
260 265 270

Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn Phe  
275 280 285

Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys Ile  
290 295 300

Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr Ala  
305 310 315 320

Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr Leu  
325 330 335

His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu Ser  
340 345 350

Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe Phe  
355 360 365

Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln Gly  
370 375 380

Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile Glu  
385 390 395 400

Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro Thr  
405 410 415

Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys Ile  
420 425 430

Val Asn Leu Asn Pro Leu Leu Leu Leu Gly Lys Leu Leu Pro Asp Asn  
435 440 445

Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu Glu  
450 455 460

Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu Lys  
465 470 475 480

Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu Asn  
485 490 495

Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile Leu  
500 505 510

Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp Ser  
515 520 525

Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly Leu  
530 535 540

Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys Glu  
545 550 555 560

Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met Glu  
565 570 575

Glu

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<211> 1416

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (3)...(1199)

<223> Clone AG5.9

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Lys Val Met Glu Glu Ala Lys Ala Phe Thr Thr Asn Tyr Leu Lys  
1 5 10 15

aaa gtt tta gca gga cgg gag gct acc cac gtc gat gaa agc ctt ttg 95  
Lys Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu  
20 25 30

gga gag gtg aag tac gca ttg gag ttt cca tgg cat tgc agt gtg cag 143  
Gly Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln  
35 40 45

aga tgg gag gca agg agc ttt atc gaa ata ttt gga caa att gat tca 191  
Arg Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser  
50 55 60

gag ctt aag tcg aat ttg agc aaa aaa atg tta gag ttg gcg aaa ttg 239  
Glu Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu  
65 70 75

gac ttc aat att ctg caa tgc aca cat cag aaa gaa ctg cag att atc 287  
Asp Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile  
80 85 90 95

tca agg tgg ttc gca gac tca agt ata gca tcc ctg aat ttc tat cgg 335  
Ser Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg  
100 105 110

aaa tgt tac gtc gaa ttt tac ttt tgg atg gct gca gcc atc tcc gag 383

Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	Ile	Ser	Glu		
115									120						125		
ccg	gag	ttt	tct	gga	agc	aga	gtt	gcc	ttc	aca	aaa	att	gct	ata	ctg	431	
Pro	Glu	Phe	Ser	Gly	Ser	Gly	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala	Ile	Leu	
130									135						140		
atg	aca	atg	cta	gat	gac	ctg	tac	gat	act	cac	gga	acc	ttg	gac	caa	479	
Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu	Asp	Gln		
145									150						155		
ctc	aaa	atc	ttt	aca	gag	gga	gtg	aga	cga	tgg	gat	gtt	tcg	ttg	gta	527	
Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser	Leu	Val		
160									165						170		
gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	tgg	tta	aag	575	
Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	Trp	Leu	Lys		
180									185						190		
aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	ggg	caa	gat	623	
Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	Gly	Gln	Asp		
195									200						205		
atg	gcg	gcc	tac	ata	aga	aaa	aat	gca	tgg	gag	cga	tac	ctt	gaa	gct	671	
Met	Ala	Ala	Tyr	Ile	Arg	Lys	Asn	Ala	Trp	Glu	Arg	Tyr	Ieu	Glu	Ala		
210									215						220		
tat	ctg	caa	gat	gcg	gaa	tgg	ata	gcc	act	gga	cat	gtc	ccc	acc	ttt	719	
Tyr	Leu	Gln	Asp	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Val	Pro	Thr	Phe		
225									230						235		
gat	gag	tac	ttg	aat	aat	ggc	aca	cca	aac	act	ggg	atg	tgt	gta	ttg	767	
Asp	Glu	Tyr	Leu	Asn	Asn	Gly	Thr	Pro	Asn	Thr	Gly	Met	Cys	Val	Leu		
240									245						250		
aat	ttg	att	ccg	ctt	ctg	tta	atg	ggt	gaa	cat	tta	cca	atc	gac	att	815	
Asn	Leu	Ile	Pro	Leu	Leu	Ieu	Met	Gly	Glu	His	Leu	Pro	Ile	Asp	Ile		
260									265						270		
ctg	gag	caa	ata	ttc	ttg	ccc	tcc	agg	ttc	cac	cat	ctc	att	gaa	ttg	863	
Leu	Glu	Gln	Ile	Phe	Leu	Pro	Ser	Arg	Phe	His	His	Leu	Ile	Glu	Leu		
275									280						285		
gct	tcc	agg	ctc	gtc	gat	gac	gcg	aga	gat	ttc	cag	gcg	gag	aag	gat	911	
Ala	Ser	Arg	Leu	Val	Asp	Asp	Ala	Arg	Asp	Phe	Gln	Ala	Glu	Lys	Asp		
290									295						300		
cat	ggg	gat	tta	tcg	tgt	att	gag	tgt	tat	tta	aaa	gat	cat	cct	gag	959	
His	Gly	Asp	Leu	Ser	Cys	Ile	Glu	Cys	Tyr	Leu	Lys	Asp	His	Pro	Glu		
305									310						315		
tct	aca	gta	gaa	gat	gct	tta	aat	cat	gtt	aat	ggc	ctc	ctt	ggc	aat	1007	
Ser	Thr	Val	Glu	Asp	Ala	Leu	Asn	His	Val	Asn	Gly	Leu	Leu	Gly	Asn		
320									325						330		
tgc	ctt	ctg	gaa	atg	aat	tgg	aag	ttc	tta	aag	aag	cag	gac	agt	gtg	1055	
Cys	Leu	Leu	Glu	Met	Asn	Trp	Lys	Phe	Leu	Lys	Lys	Gln	Asp	Ser	Val		
340									345						350		
cca	ctc	tcg	tgt	aag	aag	tac	agc	ttc	cat	gta	ttg	gca	cga	agc	atc	1103	
Pro	Leu	Ser	Cys	Lys	Lys	Tyr	Ser	Phe	His	Val	Leu	Ala	Arg	Ser	Ile		

355

360

365

caa ttc atg tac aat caa ggc gat ggc ttc tcc att tcg aac aaa gtg 1151  
Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val  
370 375 380

atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg cct att tga 1199  
Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile  
385 390 395

tagtagatac tagatagtag attagtagct attagtagttt atttcataatc aatatttact 1259  
aatgctgatg atggtaaag tccattcaga ccaatcttg gtttattgga cttaaataaa 1319  
tgaattaatt agttgtttt aaaattgtac tatttactgt tggaaataat gttttcatta 1379  
ttgaaataac tagcacaact attttagtgt ggttgat 1416

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<211> 398  
<212> PRT  
<213> *Abies grandis*

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Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu Gly  
20 25 30

Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln Arg  
35 40 45

Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu  
50 55 60

Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp  
65 70 75 80

Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser  
85 90 95

Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys  
100 105 110

Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro  
115 120 125

Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met  
130 135 140

Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu  
145 150 155 160

Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu  
165 170 175

Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr  
180 185 190

Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met  
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr  
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp  
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn  
245 250 255

Leu Ile Pro Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu  
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala  
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His  
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser  
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys  
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro  
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln  
355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile  
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile  
385 390 395

<210> 21  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide PCR primer E wherein the letter  
"n" represents an inosine residue

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223> PCR primer E wherein the letter n represents  
inosine

<400> 21  
ggngaramrr tnatggarga rgc 23

<210> 22

<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: degenerate  
oligonucleotide primer F wherein the letter "n"  
represents an inosine residue  
  
<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223> PCR primer F wherein the letter n represents  
inosine  
  
<400> 22  
garytnccary tnhbnmgntg gtgg 24  
  
<210> 23  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: degenerate  
oligonucleotide PCR primer G wherein the letter  
"n" represents an inosine residue  
  
<220>  
<221> misc\_feature  
<222> (1)..(21)  
<223> PCR primer G wherein the letter n represents  
inosine  
  
<400> 23  
ccarttnarn ccyttnacrt c 21  
  
<210> 24  
<211> 533  
<212> DNA  
<213> Abies grandis  
  
<400> 24  
ggggaaaaaa tcatggagga agctgaaatc ttctctacca aatatttaaa agaaggccctg 60  
caaaagattc cggtctccag tcttcgcga gagatcgaaa acgttttggg atatgggtgg 120  
cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtctttgg acaggacact 180  
gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240  
aacatcttc aatccttact cgcataatccg cattgcaacc cattctgaca atggacatcc 300  
cctttcctga tcataccctc aaggaagtttgcg acgtttccatc aaagcttaac gacttggcat 360  
gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420  
aagaagcttc ctctatataca ttttatatga aagacaatcc tggagttatca gaggaagatg 480

ctctcgatca tatcaacgcc atgatcagtg acgaagtcaa aggcttcaat tgg 533

<210> 25  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: conserved  
amino acid motif on which the sequence of Primer D  
was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa  
at  
position number 4 represents Ile or Tyr or Phe, Xaa at position number 6  
represents Ala or Val and Xaa at position number 8 represents Ala or Gly

<220>  
<221> SITE  
<222> (1)..(8)  
<223> conserved amino acid motif on which sequence of  
primer D was based

<400> 25  
Asp Asp Xaa Xaa Asp Xaa Tyr Xaa  
1 5

<210> 26  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: conserved  
amino acid motif on which the sequence of Primer E  
was based wherein Xaa at position 3 represents Lys or Thr, Xaa at  
position  
4 represents Val or Ile, Xaa at position 6 represents Glu or Asp

<220>  
<221> SITE  
<222> (1)..(8)  
<223> conserved amino acid sequence on which the  
sequence of primer E was based

<400> 26  
Gly Glu Xaa Xaa Met Xaa Glu Ala  
1 5

<210> 27  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: conserved  
amino acid sequence on which the sequence of  
primer F was based wherein Xaa at position 2 represents Phe or Tyr or  
Asp

Xaa at position 3 represents Ile or Leu, Xaa at position 4 represents Thr or Leu  
or Arg

<220>  
<221> SITE  
<222> (1)..(7)  
<223> conserved amino acid sequence on which the sequence of primer F was based

<400> 27  
Gln Xaa Xaa Xaa Arg Trp Trp  
1 5

<210> 28  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of primer G was based wherein Xaa at position 6 represents Phe or Leu

<220>  
<221> SITE  
<222> (1)..(8)  
<223> conserved amino acid sequence on which the sequence of primer G was based

<400> 28  
Asp Val Ile Lys Gly Xaa Asn Trp  
1 5

<210> 29  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: T3 primer oligonucleotide sequence

<400> 29  
aattaaccct cactaaaggg 20

<210> 30  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: T7 oligonucleotide primer sequence

<400> 30  
gtaataacgac tcactatagg gc 22

<210> 31  
<211> 2205  
<212> DNA  
<213> *Abies grandis*

<220>  
<221> CDS  
<222> (57)..(1943)  
<223> Clone AG3.48

<400> 31  
gttatcttga gcttcctcca tataggccaa cacatatcat atcaaaggga gcaaga atg 59  
Met  
1

gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107  
Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys  
5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155  
Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile  
20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203  
Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr Pro Ser Met  
35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251  
Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg  
50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299  
Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser  
70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347  
Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg  
85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395  
Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp  
100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443  
Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile  
115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491  
Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu  
130 135 140 145

ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc 539  
Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly  
150 155 160

att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg 587  
Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala  
165 170 175

ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag 635

Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro Glu  
180 185 190

gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta tgc tcc ccc 683  
Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser Pro  
195 200 205

ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta tat cgg gct 731  
Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg Ala  
210 215 220 225

tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa gct gaa atc 779  
Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile  
230 235 240

ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att cca gtc tcc 827  
Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val Ser  
245 250 255

gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc tgg cac aca 875  
Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His Thr  
260 265 270

aat ttg cca aga ttg gaa gca aga aat tac ata gac aca ctt gag aaa 923  
Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu Lys  
275 280 285

gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag ctt tta gaa 971  
Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu Glu  
290 295 300 305

ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa caa aag gaa 1019  
Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys Glu  
310 315 320

tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg cct aaa ttg 1067  
Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys Leu  
325 330 335

aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg gcc tct tgt 1115  
Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser Cys  
340 345 350

att gcc att gac cca aaa cat tct gca ttc aga cta ggc ttc gcc aaa 1163  
Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys  
355 360 365

atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac act ttt gga 1211  
Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly  
370 375 380 385

acg att gac gag ctt gaa ctc ttc aca tct gca att aag aga tgg aat 1259  
Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp Asn  
390 395 400

tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt gtg tac atg 1307  
Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr Met  
405 410 415

gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg gag aag act 1355  
Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys Thr

420	425	430		
caa ggg aga aac act ctc aac tat gtt cga aag gct tgg gag gct tat Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala Tyr 435	440	445	1403	
ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat ggt tat ctg Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr Leu 450	455	460	465	1451
cca acg ttt gaa gag tac cat gag aat ggg aaa gtg agc tct gca tat Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala Tyr 470	475	480	1499	
cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca tgg ctt cct Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu Pro 485	490	495	1547	
gat tac atc ttg aag gga att gat ttt cca tcc agg ttc aat gat ttg Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu 500	505	510	1595	
gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc tac aag gcc Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala 515	520	525	1643	
gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt tat atg aaa Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys 530	535	540	545	1691
gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat atc aat gcc Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala 550	555	560	1739	
atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt cta aga tcc Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg Ser 565	570	575	1787	
aac gac aat att cca atg ctg gcc aag aaa cat gct ttt gac ata aca Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile Thr 580	585	590	1835	
aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt agt gtt gcc Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val Ala 595	600	605	1883	
aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt gaa tct atg Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser Met 610	615	620	625	1931
ctt ttt taa cta taaccatatac cataataata agctcataat gctaaattat Leu Phe			1983	
tggccttatg acatagttta tttatgtact tttatgtttttaaatttataat gctaaattat ttatagat acccatgttg aataatgaat tacaaaaaga gaaattttatg tagaataaga tttggaaatgtt ttaaaaaaaaaaaaaa aaaaaaaaaaa aa			2043	
			2103	
			2163	
			2205	

<210> 32  
<211> 627  
<212> PRT  
<213> *Abies grandis*

<400> 32  
Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg  
1 5 10 15  
Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr  
20 25 30  
Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr Pro Ser  
35 40 45  
Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg  
50 55 60  
Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Phe Ile Gln  
65 70 75 80  
Ser Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu  
85 90 95  
Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp  
100 105 110  
Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp  
115 120 125  
Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn  
130 135 140  
Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn  
145 150 155 160  
Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr  
165 170 175  
Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro  
180 185 190  
Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser  
195 200 205  
Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg  
210 215 220  
Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu  
225 230 235 240  
Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val  
245 250 255  
Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His  
260 265 270  
Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu  
275 280 285

Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu  
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys  
305 310 315 320

Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys  
325 330 335

Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser  
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala  
355 360 365

Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe  
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp  
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr  
405 410 415

Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys  
420 425 430

Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala  
435 440 445

Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr  
450 455 460

Leu Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala  
465 470 475 480

Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu  
485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp  
500 505 510

Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys  
515 520 525

Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met  
530 535 540

Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn  
545 550 555 560

Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg  
565 570 575

Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile  
580 585 590

Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val  
595 600 605

Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser

610

615

620

Met Leu Phe  
625

<210> 33  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 2.2 BamHI

<400> 33  
caaaggatc cagaatggct ctgg 24

<210> 34  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 2.2 Not I

<400> 34  
agtaagcggc cgcttttaa tcataacccac 30

<210> 35  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 3.18 EcoRI

<400> 35  
ctgcaggaat tcggcacgag c 21

<210> 36  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 3.18 SmaI

<400> 36  
catagcccg ggcatacatt tgagctg 27

<210> 37  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 10 NdeI

<400> 37

ggcaggaaca tatggctctc ctttctatcg

30

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 10 BamHI

<400> 38

tctagaacta gtggatcccc cgggctgcag

30

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer JB29

<400> 39

ctaccattcc aatatctg

18

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 2-8

<400> 40

gttggatctt agaagttccc

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 3-9

<400> 41

tttccattcc aacctctggg

20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 3-11

<400> 42 20  
cgtaatggaa agctctggcg

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 7-1

<400> 43 20  
ccttacacgc ctttggatgg

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR  
oligonucleotide sequence 7-3

<400> 44 20  
tctgttgc caggatggc

<210> 45  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: conserved  
amino acid motif common to all prenyl transferases wherein Xaa at  
position  
3 and 4 represents any amino acid

<400> 45  
Asp Asp Xaa Xaa Asp  
1 5

<210> 46  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide primers can be synthesized that hybridize to the monoterpenes synthases of the present invention, wherein Xaa at position 4 represents

Leu or Ile or Val

<400> 46

His Ser Asn Xaa Trp Asp Asp Asp  
1 5

<210> 47

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotides can be constructed that hybridize to the monoterpenes synthases of the present invention

<400> 47

Ala Leu Asp Tyr Val Tyr  
1 5

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to the monoterpenes synthases of the present invention

<400> 48

Glu Leu Ala Lys Leu Glu Phe  
1 5

<210> 49

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to monoterpenes synthase clones of the present invention

<400> 49

Arg Trp Trp Lys Glu Ser  
1 5

<210> 50  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to monoterpane synthase clones of the present invention, wherein Xaa at position 1 represents Val or Ile or Leu

<400> 50  
Xaa Leu Asp Asp Met Tyr Asp  
1 5

<210> 51  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to monoterpane synthase clones of the present invention wherein Xaa at position 1 reperesents Val or Ile or Leu

<400> 51  
Xaa Leu Asp Asp Leu Tyr Asp  
1 5

<210> 52  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpane synthase clones of the present invention, wherein Xaa at position 1 represents Val or Ile or Leu

<400> 52  
Xaa Leu Asp Asp Ile Tyr Asp  
1 5

<210> 53  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid

motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpene synthase clones of the present invention, wherein Xaa at position 6 represents Asn or His

<400> 53  
Cys Tyr Met Lys Asp Xaa Pro  
1 . 5

<210> 54  
<211> 9  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet

<400> 54  
atgatgatg 9

<210> 55  
<211> 9  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: exemplary oligonucleotide sequence that corresponds to peptide sequence MetMetMet

<400> 55  
tactactac 9

<210> 56  
<211> 9  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet, n is inosine

<400> 56  
nacnacnac 9

<210> 57  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide corresponding to amino acid sequence set forth in SEQ ID NO:46

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223> Oligonucleotide that corresponds to the conserved  
amino acid sequence set forth in SEQ ID NO:46

<400> 57  
gtgtcggtgg agaccctgct gctg

24

<210> 58  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide sequence corresponding to amino  
acid sequence set forth in SEQ ID NO:47

<220>  
<221> misc\_feature  
<222> (1)..(18)  
<223> Oligonucleotide corresponding to amino acid  
sequence set forth in SEQ ID NO:47

<400> 58  
cgggagctga tgcagatg

18

<210> 59  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide that corresponds to amino acid  
sequence set forth in SEQ ID NO:48

<220>  
<221> misc\_feature  
<222> (1)..(21)  
<223> Oligonucleotide that corresponds to conserved  
amino acid sequence set forth in SEQ ID NO:48

<400> 59  
ctcgagcggt tcgagctcaa g

21

<210> 60  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide that corresponds to amino acid  
sequence set forth in SEQ ID NO:49

<220>  
<221> misc\_feature  
<222> (1)..(18)  
<223> Oligonucleotide that corresponds to conserved  
amino acid sequence set forth in SEQ ID NO:49

<400> 60  
gccaccacct tcctctcg 18

<210> 61  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide sequence corresponding to amino  
acid sequence set forth in SEQ ID NO:50

<220>  
<221> misc\_feature  
<222> (1)..(21)  
<223> Oligonucleotide sequence corresponding to amino  
acid sequence set forth in SEQ ID NO:50

<400> 61  
gaggagctgc tgtacatgct g 21

<210> 62  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide corresponding to amino acid  
sequence set forth in SEQ ID NO:51

<220>  
<221> misc\_feature  
<222> (1)..(21)  
<223> Oligonucleotide corresponding to conserved amino  
acid sequence set forth in SEQ ID NO:51

<400> 62  
gaggagctgc tggagatgct g 21

<210> 63  
<211> 293  
<212> DNA  
<213> Abies grandis

<400> 63  
cttaatgaat tggcgcaaga ggctgagaag actcaaggca gagatacgct caactatatt 60  
cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

ggttatctcc caacgtttga ggagtacttg aagaatggga aagtttagttc cggttctcg 180  
acagccactt tacaaccat actcaccttg gatgtaccac ttccctaatta catactgcaa 240  
gaaattgatt atccatctag gttcaatgac ttggcttcgt ccctccttcg cta 293

<210> 64  
<211> 2013  
<212> DNA  
<213> *Abies grandis*

<220>  
<221> CDS  
<222> (36)..(1889)

<400> 64  
tttgacgtg ctttcttatac tgatagcaag ctgaa atg gct ctt ctt tct att 53  
Met Ala Leu Leu Ser Ile  
1 5  
act ccg ctg gtt tcc agg tcg tgc ctc agt tct tct cat gag att aag 101  
Thr Pro Leu Val Ser Arg Ser Cys Leu Ser Ser His Glu Ile Lys  
10 15 20  
gct ctc cgt aga aca atc cca act ctt gga atc tgc agg ccg ggg aaa 149  
Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly Ile Cys Arg Pro Gly Lys  
25 30 35  
tcc gtc gcg cat tcc ata aac atg tgt ttg aca agc gtc gca tct act 197  
Ser Val Ala His Ser Ile Asn Met Cys Leu Thr Ser Val Ala Ser Thr  
40 45 50  
gat tct gta cag aga cgc gtg ggc aac tat cat tcc aac ctg tgg gac 245  
Asp Ser Val Gln Arg Arg Val Gly Asn Tyr His Ser Asn Leu Trp Asp  
55 60 65 70  
gat gat ttc ata cag tct ctg atc tca acg cct tat gga gca cct gat 293  
Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr Pro Tyr Gly Ala Pro Asp  
75 80 85  
tac cgg gaa cgt gct gac aga ctt att ggg gaa gta aag gat ata atg 341  
Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly Glu Val Lys Asp Ile Met  
90 95 100  
ttc aat ttc aag tcg ctg gaa gat gga ggc aat gat ctc ctt caa cga 389  
Phe Asn Phe Lys Ser Leu Glu Asp Gly Asn Asp Leu Leu Gln Arg  
105 110 115  
ctt ttg ctg gtc gat gac gtt gaa cgt ttg gga atc gac agg cat ttc 437  
Leu Leu Leu Val Asp Asp Val Glu Arg Leu Gly Ile Asp Arg His Phe  
120 125 130  
aaa aaa gag ata aaa acg gca ctc gat tat gtt aac agt tat tgg aac 485  
Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr Val Asn Ser Tyr Trp Asn  
135 140 145 150  
gaa aaa ggc att gga tgt ggg agg gag agt gtt gtg act gac ctc aac 533  
Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn  
155 160 165

tca acc gcc ttg ggg ctt cga act ctc cga cta cac gga tac act gtg Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Thr Val 170	175	180	581	
tct tca gat ttg aac gtt ttt aaa gac aaa aat ggg caa ttt tcc Ser Ser Asp Val Leu Asn Val Phe Lys Asp Lys Asn Gly Gln Phe Ser 185	190	195	629	
tcc act gcc aat att cag ata gag gga gag att aga ggc gtt ctc aat Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu Ile Arg Gly Val Leu Asn 200	205	210	677	
tta ttc agg gcc tcc ctc gtc gcc ttt ccc ggc gag aaa gtt atg gat Leu Phe Arg Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Asp 215	220	225	230	725
gaa gct gaa aca ttc tct aca aaa tat tta aga gaa gcc ctg caa aag Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu Arg Glu Ala Leu Gln Lys 235	240	245	773	
att ccg gca tcc agt ata ctt tca cta gag ata cgg gac gtt ctg gaa Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu Ile Arg Asp Val Leu Glu 250	255	260	821	
tat ggt tgg cac acc aat ttg cca cgc ttg gaa gca agg aat tac atg Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Met 265	270	275	869	
gac gtc ttt gga cag cac act aaa aat aag aac gcc gcc gag aaa ctt Asp Val Phe Gly Gln His Thr Lys Asn Lys Asn Ala Ala Glu Lys Leu 280	285	290	917	
tta gaa ctt gca aaa ttg gaa ttc aat ata ttt cac tcc tta caa gag Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Glu 295	300	305	310	965
aga gag tta aaa cat gtt tcc cga tgg tgg aaa gac tcg ggt tct cct Arg Glu Leu Lys His Val Ser Arg Trp Trp Lys Asp Ser Gly Ser Pro 315	320	325	1013	
gag atg acc ttc tgt cga cat cgt cac gtg gaa tac tac gct ttg gct Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Ala Leu Ala 330	335	340	1061	
tcc tgc att gcg ttc gag cct caa cat tct gga ttc aga ctc ggc ttt Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly Phe 345	350	355	1109	
acc aag atg tct cat ctt atc acg gtt ctt gac gac atg tac gac gtc Thr Lys Met Ser His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp Val 360	365	370	1157	
ttc ggc aca gta gac gag ctg gaa ctc ttc aca gcg aca att aag aga Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Ile Lys Arg 375	380	385	390	1205
tgg gat ccg tcc gcg atg gaa tgc ctt cca gaa tat atg aaa gga gtg Trp Asp Pro Ser Ala Met Glu Cys Leu Pro Glu Tyr Met Lys Gly Val 395	400	405	1253	
tac atg atg gtt tat cac acc gta aat gaa atg gct cga gtg gca gag			1301	

Tyr Met Met Val Tyr His Thr Val Asn Glu Met Ala Arg Val Ala Glu  
410 415 420

aag gct caa ggc cga gac acg ctc aac tat gca aga cag gct tgg gag 1349  
Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Gln Ala Trp Glu  
425 430 435

gcg tgt ttt gat tcg tat atg cag gaa gca aag tgg atc gcc act ggt 1397  
Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala Lys Trp Ile Ala Thr Gly  
440 445 450

tat ctg ccc acg ttt gag gag tac ttg gag aac ggg aaa gtt agc tct 1445  
Tyr Leu Pro Thr Phe Glu Tyr Leu Glu Asn Gly Lys Val Ser Ser  
455 460 465 470

gct cat cgc cca tgc gca ctg caa ccc att ctg acg ttg gac atc ccc 1493  
Ala His Arg Pro Cys Ala Leu Gln Pro Ile Leu Thr Leu Asp Ile Pro  
475 480 485

ttt cct gat cac atc ctc aag gaa gtt gac ttc cca tcg aag ctc aat 1541  
Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn  
490 495 500

gac ttg ata tgt atc atc ctt cga tta aga ggt gat aca cgg tgc tac 1589  
Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr  
505 510 515

aag gca gac agg gcc cgt gga gaa gaa gct tcg tct ata tca tgt tat 1637  
Lys Ala Asp Arg Ala Arg Gly Glu Ala Ser Ser Ile Ser Cys Tyr  
520 525 530

atg aaa gac aat cct gga tta acg gaa gaa gat gct ctg aat cat atc 1685  
Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Ala Leu Asn His Ile  
535 540 545 550

aac ttc atg atc agg gac gca atc aga gaa tta aat tgg gag ctt cta 1733  
Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu  
555 560 565

aag cca gac aac agt gtt ccc atc act tcc aag aaa cac gca ttt gac 1781  
Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp  
570 575 580

ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc 1829  
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser  
585 590 595

ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa 1877  
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu  
600 605 610

cct gtg cct ttg taacaacact tcaaatctac aatattaact gaggatgcc 1929  
Pro Val Pro Leu  
615

tatgggtgta tatagggcac acaaaaataa atatggttgt gtttagtaaag ctgtaattta 1989

tgaaaaaaaaaaaaaaaaaaaa 2013

<211> 618  
<212> PRT  
<213> Abies grandis

<400> 65  
Met Ala Leu Leu Ser Ile Thr Pro Leu Val Ser Arg Ser Cys Leu Ser  
1 5 10 15  
Ser Ser His Glu Ile Lys Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly  
20 25 30  
Ile Cys Arg Pro Gly Lys Ser Val Ala His Ser Ile Asn Met Cys Leu  
35 40 45  
Thr Ser Val Ala Ser Thr Asp Ser Val Gln Arg Arg Val Gly Asn Tyr  
50 55 60  
His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr  
65 70 75 80  
Pro Tyr Gly Ala Pro Asp Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly  
85 90 95  
Glu Val Lys Asp Ile Met Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly  
100 105 110  
Asn Asp Leu Leu Gln Arg Leu Leu Val Asp Asp Val Glu Arg Leu  
115 120 125  
Gly Ile Asp Arg His Phe Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr  
130 135 140  
Val Asn Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser  
145 150 155 160  
Val Val Thr Asp Leu Asn Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg  
165 170 175  
Leu His Gly Tyr Thr Val Ser Ser Asp Val Leu Asn Val Phe Lys Asp  
180 185 190  
Lys Asn Gly Gln Phe Ser Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu  
195 200 205  
Ile Arg Gly Val Leu Asn Leu Phe Arg Ala Ser Leu Val Ala Phe Pro  
210 215 220  
Gly Glu Lys Val Met Asp Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu  
225 230 235 240  
Arg Glu Ala Leu Gln Lys Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu  
245 250 255  
Ile Arg Asp Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu  
260 265 270  
Glu Ala Arg Asn Tyr Met Asp Val Phe Gly Gln His Thr Lys Asn Lys  
275 280 285  
Asn Ala Ala Glu Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile  
290 295 300

Phe His Ser Leu Gln Glu Arg Glu Leu Lys His Val Ser Arg Trp Trp  
305 310 315 320

Lys Asp Ser Gly Ser Pro Glu Met Thr Phe Cys Arg His Arg His Val  
325 330 335

Glu Tyr Tyr Ala Leu Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser  
340 345 350

Gly Phe Arg Leu Gly Phe Thr Lys Met Ser His Leu Ile Thr Val Leu  
355 360 365

Asp Asp Met Tyr Asp Val Phe Gly Thr Val Asp Glu Leu Glu Leu Phe  
370 375 380

Thr Ala Thr Ile Lys Arg Trp Asp Pro Ser Ala Met Glu Cys Leu Pro  
385 390 395 400

Glu Tyr Met Lys Gly Val Tyr Met Met Val Tyr His Thr Val Asn Glu  
405 410 415

Met Ala Arg Val Ala Glu Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr  
420 425 430

Ala Arg Gln Ala Trp Glu Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala  
435 440 445

Lys Trp Ile Ala Thr Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu  
450 455 460

Asn Gly Lys Val Ser Ser Ala His Arg Pro Cys Ala Leu Gln Pro Ile  
465 470 475 480

Leu Thr Leu Asp Ile Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp  
485 490 495

Phe Pro Ser Lys Leu Asn Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg  
500 505 510

Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala  
515 520 525

Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu  
530 535 540

Asp Ala Leu Asn His Ile Asn Phe Met Ile Arg Asp Ala Ile Arg Glu  
545 550 555 560

Leu Asn Trp Glu Leu Leu Lys Pro Asp Asn Ser Val Pro Ile Thr Ser  
565 570 575

Lys Lys His Ala Phe Asp Ile Ser Arg Val Trp His His Gly Tyr Arg  
580 585 590

Tyr Arg Asp Gly Tyr Ser Phe Ala Asn Val Glu Thr Lys Ser Leu Val  
595 600 605

Met Arg Thr Val Ile Glu Pro Val Pro Leu  
610 615

<210> 66  
<211> 2186  
<212> DNA  
<213> *Abies grandis*

<220>  
<221> CDS  
<222> (34)..(1923)

<400> 66  
cccaaatcct atatccgtta taagcgagca gga atg gct ctg gtt tct tcc gca 54  
Met Ala Leu Val Ser Ser Ala  
1 5  
  
ccc aaa tcc tgc ctg cac aaa tcg ttg atc agg tct act cat cat gag 102  
Pro Lys Ser Cys Leu His Lys Ser Leu Ile Arg Ser Thr His His Glu  
10 15 20  
  
ctc aag cct ctg cgc aga acc atc cca act ctt gga atg tgt agg cga 150  
Leu Lys Pro Leu Arg Arg Thr Ile Pro Thr Leu Gly Met Cys Arg Arg  
25 30 35  
  
ggg aaa tct ttc aca cct tct gtg agc atg agt ttg acc acc gct gta 198  
Gly Lys Ser Phe Thr Pro Ser Val Ser Met Ser Leu Thr Thr Ala Val  
40 45 50 55  
  
tct gat gat ggt cta caa aga cgc ata ggt gac tat cat tcc aat ctc 246  
Ser Asp Asp Gly Leu Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Leu  
60 65 70  
  
tgg gac gac gat ttc ata cag tct cta tca acg cct tat ggg gag cct 294  
Trp Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro  
75 80 85  
  
tct tac cga gaa cgt gct gag aaa ctg att ggg gaa gtg aag gag atg 342  
Ser Tyr Arg Glu Arg Ala Glu Lys Leu Ile Gly Glu Val Lys Glu Met  
90 95 100  
  
ttc aat tca atg cca tcg gaa gat gga gaa tca atg agt ccc ctc aat 390  
Phe Asn Ser Met Pro Ser Glu Asp Gly Glu Ser Met Ser Pro Leu Asn  
105 110 115  
  
gat ctt att gaa cga ctt tgg atg gtc gat agc gtt gaa cgt ttg ggg 438  
Asp Leu Ile Glu Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly  
120 125 130 135  
  
att gat aga cat ttc aaa aaa gag ata aaa tca gcc ctt gat tat gtt 486  
Ile Asp Arg His Phe Lys Lys Glu Ile Lys Ser Ala Leu Asp Tyr Val  
140 145 150  
  
tac agt tat tgg aac gaa aaa ggt att gga tgc ggt aga gat agt gtt 534  
Tyr Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Asp Ser Val  
155 160 165  
  
ttt cct gat gtc aac tcg act gcc tcg ggg ttt cga act ctt cgc cta 582  
Phe Pro Asp Val Asn Ser Thr Ala Ser Gly Phe Arg Thr Leu Arg Leu  
170 175 180  
  
cac gga tac agt gtc tct tca gag gtt ttg aaa gta ttt caa gac caa 630  
His Gly Tyr Ser Val Ser Glu Val Leu Lys Val Phe Gln Asp Gln

185	190	195	
aat ggg cag ttt gca ttc tct cct agt aca aaa gag aga gac atc aga			678
Asn Gly Gln Phe Ala Phe Ser Pro Ser Thr Lys Glu Arg Asp Ile Arg			
200	205	210	215
acc gtt ctg aat tta tat cgg gct tct ttc att gcc ttt cct ggg gag			726
Thr Val Leu Asn Leu Tyr Arg Ala Ser Phe Ile Ala Phe Pro Gly Glu			
220	225	230	
aaa gtt atg gaa gag gct gaa att ttc tct tca aga tat ttg aaa gaa			774
Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ser Arg Tyr Leu Lys Glu			
235	240	245	
gcc gtg caa aag att ccg gtc tcc agt ctt tca caa gaa ata gac tac			822
Ala Val Gln Lys Ile Pro Val Ser Ser Leu Ser Gln Glu Ile Asp Tyr			
250	255	260	
act ttg gaa tat ggt tgg cac aca aat atg cca aga ttg gaa aca agg			870
Thr Leu Glu Tyr Gly Trp His Thr Asn Met Pro Arg Leu Glu Thr Arg			
265	270	275	
aat tac tta gat gta ttt gga cat cct acc agt cca tgg ctc aag aag			918
Asn Tyr Leu Asp Val Phe Gly His Pro Thr Ser Pro Trp Leu Lys Lys			
280	285	290	295
aaa agg acg caa tat ctg gac agc gaa aag ctt tta gaa ctc gca aaa			966
Lys Arg Thr Gln Tyr Leu Asp Ser Glu Lys Leu Leu Glu Leu Ala Lys			
300	305	310	
ttg gag ttc aac atc ttt cac tcc ctt caa cag aag gag tta cag tat			1014
Leu Glu Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr			
315	320	325	
ctc tcc aga tgg tgg ata cat tcg ggt ttg cct gaa ctg acc ttt ggt			1062
Leu Ser Arg Trp Trp Ile His Ser Gly Leu Pro Glu Leu Thr Phe Gly			
330	335	340	
cgg cat cgt cac gtg gaa tac tac acc ctg agc tct tgc att gcg act			1110
Arg His Arg His Val Glu Tyr Tyr Thr Leu Ser Ser Cys Ile Ala Thr			
345	350	355	
gag ccc aaa cat tct gca ttc aga ttg ggc ttt gcc aaa acg tgt cat			1158
Glu Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys Thr Cys His			
360	365	370	375
ctt atc acg gtt ctg gac gat atc tac gac act ttc gga acg atg gat			1206
Leu Ile Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asp			
380	385	390	
gaa atc gaa ctc ttc aac gag gca gtt agg aga tgg aat ccg tcg gag			1254
Glu Ile Glu Leu Phe Asn Glu Ala Val Arg Arg Trp Asn Pro Ser Glu			
395	400	405	
aaa gaa cgc ctc cca gaa tat atg aaa gaa atc tac atg gca ctc tac			1302
Lys Glu Arg Leu Pro Glu Tyr Met Lys Glu Ile Tyr Met Ala Leu Tyr			
410	415	420	
gaa gcc tta act gac atg gcg cga gag gca gag aag aca caa ggc cga			1350
Glu Ala Leu Thr Asp Met Ala Arg Glu Ala Glu Lys Thr Gln Gly Arg			
425	430	435	

gac acg ctc aat tat gct aga aag gct tgg gaa gtt tat ctt gat tcg 1398  
Asp Thr Leu Asn Tyr Ala Arg Lys Ala Trp Glu Val Tyr Leu Asp Ser  
440 445 450 455

tat aca caa gaa gca aag tgg atc gcc agc ggt tat ctg cca act ttc 1446  
Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe  
460 465 470

gag gag tac tta gag aac gcg aag gtt agc tct ggt cat cgt gca gcg 1494  
Glu Glu Tyr Leu Glu Asn Ala Lys Val Ser Ser Gly His Arg Ala Ala  
475 480 485

gca ttg aca ccc ctc ctg aca ttg gac gta ccg ctt cct gat gac gtc 1542  
Ala Leu Thr Pro Leu Leu Thr Leu Asp Val Pro Leu Pro Asp Asp Val  
490 495 500

ttg aag gga ata gat ttt cca tcg aga ttt aat gat ttg gca tct tcc 1590  
Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser  
505 510 515

ttc ctt aga cta aga ggt gac aca cga tgc tac aag gca gac agg gac 1638  
Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Asp  
520 525 530 535

cga gga gaa gaa gcg tca agc ata tcg tgt tac atg aaa gac aat ccc 1686  
Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro  
540 545 550

gga tta aca gag gaa gat gct ctc aat cat atc aat gcc atg atc aac 1734  
Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn  
555 560 565

gac ata atc aaa gaa tta aat tgg gaa ctt ctc aaa ccc gat agc aat 1782  
Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn  
570 575 580

att cca atg act gca cgg aaa cat gct tat gag ata acc aga gct ttc 1830  
Ile Pro Met Thr Ala Arg Lys His Ala Tyr Glu Ile Thr Arg Ala Phe  
585 590 595

cac caa ctt tac aaa tat aga gat ggc ttc agc gtt gcc actcaa gaa 1878  
His Gln Leu Tyr Lys Tyr Arg Asp Gly Phe Ser Val Ala Thr Gln Glu  
600 605 610 615

acg aaa agt ttg gtg agg aga acg gtc ctt gaa cca gtg cct ctt 1923  
Thr Lys Ser Leu Val Arg Arg Thr Val Leu Glu Pro Val Pro Leu  
620 625 630

taacaattta aaccttctat aataaattgg tggtaggtcc gctatgcgtt tatgcatttg 1983  
catgtctctc tatgtaacta gttgtatgctg tggatgatt ataaaaattgg aggttactcg 2043  
gtcctcacat ggtaatatgt gagttgtgaa attctaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2103  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2163  
aaaaaaaaaaa aaaaaaaaaaaa aaa 2186

<211> 630  
<212> PRT  
<213> *Abies grandis*

<400> 67  
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1 5 10 15  
Ile Arg Ser Thr His His Glu Leu Lys Pro Leu Arg Arg Thr Ile Pro  
20 25 30  
Thr Leu Gly Met Cys Arg Arg Gly Lys Ser Phe Thr Pro Ser Val Ser  
35 40 45  
Met Ser Leu Thr Thr Ala Val Ser Asp Asp Gly Leu Gln Arg Arg Ile  
50 55 60  
Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu  
65 70 75 80  
Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Arg Glu Arg Ala Glu Lys Leu  
85 90 95  
Ile Gly Glu Val Lys Glu Met Phe Asn Ser Met Pro Ser Glu Asp Gly  
100 105 110  
Glu Ser Met Ser Pro Leu Asn Asp Leu Ile Glu Arg Leu Trp Met Val  
115 120 125  
Asp Ser Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys Lys Glu Ile  
130 135 140  
Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu Lys Gly Ile  
145 150 155 160  
Gly Cys Gly Arg Asp Ser Val Phe Pro Asp Val Asn Ser Thr Ala Ser  
165 170 175  
Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Ser Val Ser Ser Glu Val  
180 185 190  
Leu Lys Val Phe Gln Asp Gln Asn Gly Gln Phe Ala Phe Ser Pro Ser  
195 200 205  
Thr Lys Glu Arg Asp Ile Arg Thr Val Leu Asn Leu Tyr Arg Ala Ser  
210 215 220  
Phe Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe  
225 230 235 240  
Ser Ser Arg Tyr Leu Lys Glu Ala Val Gln Lys Ile Pro Val Ser Ser  
245 250 255  
Leu Ser Gln Glu Ile Asp Tyr Thr Leu Glu Tyr Gly Trp His Thr Asn  
260 265 270  
Met Pro Arg Leu Glu Thr Arg Asn Tyr Leu Asp Val Phe Gly His Pro  
275 280 285  
Thr Ser Pro Trp Leu Lys Lys Lys Arg Thr Gln Tyr Leu Asp Ser Glu  
290 295 300

Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu  
305 310 315 320

Gln Gln Lys Glu Leu Gln Tyr Leu Ser Arg Trp Trp Ile His Ser Gly  
325 330 335

Leu Pro Glu Leu Thr Phe Gly Arg His Arg His Val Glu Tyr Tyr Thr  
340 345 350

Leu Ser Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe Arg Leu  
355 360 365

Gly Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr  
370 375 380

Asp Thr Phe Gly Thr Met Asp Glu Ile Glu Leu Phe Asn Glu Ala Val  
385 390 395 400

Arg Arg Trp Asn Pro Ser Glu Lys Glu Arg Leu Pro Glu Tyr Met Lys  
405 410 415

Glu Ile Tyr Met Ala Leu Tyr Glu Ala Leu Thr Asp Met Ala Arg Glu  
420 425 430

Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Lys Ala  
435 440 445

Trp Glu Val Tyr Leu Asp Ser Tyr Thr Gln Glu Ala Lys Trp Ile Ala  
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Ala Lys Val  
465 470 475 480

Ser Ser Gly His Arg Ala Ala Leu Thr Pro Leu Leu Thr Leu Asp  
485 490 495

Val Pro Leu Pro Asp Asp Val Leu Lys Gly Ile Asp Phe Pro Ser Arg  
500 505 510

Phe Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg  
515 520 525

Cys Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Ser Ile Ser  
530 535 540

Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn  
545 550 555 560

His Ile Asn Ala Met Ile Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu  
565 570 575

Leu Leu Lys Pro Asp Ser Asn Ile Pro Met Thr Ala Arg Lys His Ala  
580 585 590

Tyr Glu Ile Thr Arg Ala Phe His Gln Leu Tyr Lys Tyr Arg Asp Gly  
595 600 605

Phe Ser Val Ala Thr Gln Glu Thr Lys Ser Leu Val Arg Arg Thr Val  
610 615 620

Leu Glu Pro Val Pro Leu  
625 630

<210> 68  
<211> 2429  
<212> DNA  
<213> Abies grandis

<220>  
<221> CDS  
<222> (35)..(1945)

<400> 68  
attnaagaag ctaccatagt ttaggcagga atgc atg gct ctc ctt tct atc gta 55  
Met Ala Leu Leu Ser Ile Val  
1 5

tct ttg cag gtt ccc aaa tcc tgc ggg ctg aaa tcg ttg atc agt tcc 103  
Ser Leu Gln Val Pro Lys Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser  
10 15 20

agc aat gtg cag aag gct ctc tgt atc tct aca gca gtc cca act ctc 151  
Ser Asn Val Gln Lys Ala Leu Cys Ile Ser Thr Ala Val Pro Thr Leu  
25 30 35

aga atg cgt agg cga cag aaa gct ctg gtc atc aac atg aaa ttg acc 199  
Arg Met Arg Arg Arg Gln Lys Ala Leu Val Ile Asn Met Lys Leu Thr  
40 45 50 55

act gta tcc cat cgt gat gat aat ggt ggt gta ctg caa aga cgc 247  
Thr Val Ser His Arg Asp Asp Asn Gly Gly Val Leu Gln Arg Arg  
60 65 70

ata gcc gat cat cat ccc aac ctg tgg gaa gat gat ttc ata caa tca 295  
Ile Ala Asp His His Pro Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser  
75 80 85

ttg tcc tca cct tat ggg gga tct tcg tac agt gaa cgt gct gtg aca 343  
Leu Ser Ser Pro Tyr Gly Gly Ser Ser Tyr Ser Glu Arg Ala Val Thr  
90 95 100

gtg gtt gag gaa gta aaa gag atg ttc aat tca ata cca aat aat aga 391  
Val Val Glu Glu Val Lys Glu Met Phe Asn Ser Ile Pro Asn Asn Arg  
105 110 115

gaa tta ttt ggt tcc caa aat gat ctc ctt aca cgc ctt tgg atg gtg 439  
Glu Leu Phe Gly Ser Gln Asn Asp Leu Leu Thr Arg Leu Trp Met Val  
120 125 130 135

gat agc att gaa cgt ctg ggg ata gat aga cat ttc caa aat gag ata 487  
Asp Ser Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Asn Glu Ile  
140 145 150

aga gta gcc ctc gat tat gtt tac agt tat tgg aag gaa aag gaa ggc 535  
Arg Val Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly  
155 160 165

att ggg tgt ggc aga gat tct act ttt cct gat ctc aac tcg act gct 583  
Ile Gly Cys Gly Arg Asp Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala  
170 175 180

ctg gcg ctt cga act ctt cga ctg cac gga tac aat gtg tct tca gat Leu Ala Leu Arg Thr Leu Arg Leu His Gly Tyr Asn Val Ser Ser Asp 185 190 195	631
gtg ctg gaa tac ttc aaa gat caa aag ggg cat ttt gcc tgc cct gca Val Leu Glu Tyr Phe Lys Asp Gln Lys Gly His Phe Ala Cys Pro Ala 200 205 210 215	679
atc cta acc gag gga cag atc act aga agt gtt cta aat tta tat cgg Ile Leu Thr Glu Gly Gln Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg 220 225 230	727
gct tcc ctg gtc gcc ttt ccg ggg gag aaa gtt atg gaa gag gct gaa Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Glu Ala Glu 235 240 245	775
atc ttc tcg gca tct tat ttg aaa gaa gtc tta caa aag att cca gtc Ile Phe Ser Ala Ser Tyr Leu Lys Glu Val Leu Gln Lys Ile Pro Val 250 255 260	823
tcc agt ttt tca cga gag ata gaa tac gtt ttg gaa tat ggt tgg cac Ser Ser Phe Ser Arg Glu Ile Glu Tyr Val Leu Glu Tyr Gly Trp His 265 270 275	871
aca aat ttg cca aga ttg gaa gca aga aat tat atc gac gtc tac ggg Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Val Tyr Gly 280 285 290 295	919
cag gac agc tat gaa agt tca aac gag atg cca tat gtg aat acg cag Gln Asp Ser Tyr Glu Ser Ser Asn Glu Met Pro Tyr Val Asn Thr Gln 300 305 310	967
aag ctt tta aaa ctt gca aaa ttg gag ttt aat atc ttt cac tct ttg Lys Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu 315 320 325	1015
caa cag aaa gag ttg caa tat atc tct aga tgg tgg aaa gat tcg tgt Gln Gln Lys Glu Leu Gln Tyr Ile Ser Arg Trp Trp Lys Asp Ser Cys 330 335 340	1063
tca tct cat ctg act ttt act cga cac cgt cac gtg gaa tac tac aca Ser Ser His Leu Thr Phe Thr Arg His Arg His Val Glu Tyr Tyr Thr 345 350 355	1111
atg gca tct tgc att tct atg gag ccg aaa cac tcc gct ttc aga ttg Met Ala Ser Cys Ile Ser Met Glu Pro Lys His Ser Ala Phe Arg Leu 360 365 370 375	1159
ggg ttt gtc aaa aca tgt cat ctt cta aca gtt ctg gat gat atg tat Gly Phe Val Lys Thr Cys His Leu Leu Thr Val Leu Asp Asp Met Tyr 380 385 390	1207
gac act ttt gga aca ctg gac gaa ctc caa ctt ttt acg act gcc ttt Asp Thr Phe Gly Thr Leu Asp Glu Leu Gln Leu Phe Thr Thr Ala Phe 395 400 405	1255
aag aga tgg gat ttg tca gag aca aag tgt ctt cca gaa tat atg aaa Lys Arg Trp Asp Leu Ser Glu Thr Lys Cys Leu Pro Glu Tyr Met Lys 410 415 420	1303

gca gtg tac atg gac ttg tat caa tgt ctt aat gaa ttg gcg caa gag 1351  
Ala Val Tyr Met Asp Leu Tyr Gln Cys Leu Asn Glu Leu Ala Gln Glu  
425 430 435

gct gag aag act caa ggc aga gat acg ctc aac tat att cgc aat gct 1399  
Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ile Arg Asn Ala  
440 445 450 455

tat gag tct cat ttt gat tcg ttt atg cac gaa gca aaa tgg atc tca 1447  
Tyr Glu Ser His Phe Asp Ser Phe Met His Glu Ala Lys Trp Ile Ser  
460 465 470

agt ggt tat ctc cca acg ttt gag gag tac ttg aag aat ggg aaa gtt 1495  
Ser Gly Tyr Leu Pro Thr Phe Glu Tyr Leu Lys Asn Gly Lys Val  
475 480 485

agt tcc ggt tct cgc aca gcc act tta caa ccc ata ctc acc ttg gat 1543  
Ser Ser Gly Ser Arg Thr Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp  
490 495 500

gta cca ctt cct aat tac ata ctg caa gaa att gat tat cca tct agg 1591  
Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg  
505 510 515

ttc aat gac ttg gct tcg tcc ctc ctt cgg cta cgt ggt gac acg cgc 1639  
Phe Asn Asp Leu Ala Ser Ser Leu Leu Arg Leu Arg Gly Asp Thr Arg  
520 525 530 535

tgc tac aag gcg gat agg gct cgt gga gaa gaa gct tca gct ata tcg 1687  
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Ala Ser Ala Ile Ser  
540 545 550

tgt tat atg aaa gac cat cct gga tca aca gag gaa gat gct ctc aat 1735  
Cys Tyr Met Lys Asp His Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn  
555 560 565

cat atc aac gtc atg atc agt gat gca atc aga gaa tta aat tgg gag 1783  
His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu  
570 575 580

ctt ctc aga cca gat agc aaa agt ccc atc tct tcc aag aaa cat gct 1831  
Leu Leu Arg Pro Asp Ser Lys Ser Pro Ile Ser Ser Lys Lys His Ala  
585 590 595

ttt gac atc acc aga gct ttc cat cac ctc tac aag tac cga gat ggt 1879  
Phe Asp Ile Thr Arg Ala Phe His His Leu Tyr Lys Tyr Arg Asp Gly  
600 605 610 615

tac act gtt gcg agt agt gaa aca aag aat ttg gtg atg aaa aca gtt 1927  
Tyr Thr Val Ala Ser Ser Glu Thr Lys Asn Leu Val Met Lys Thr Val  
620 625 630

ctt gaa cct gtg gca ttg taaaaaaaaata tcaaccgcataaaaaatgcac 1975  
Leu Glu Pro Val Ala Leu  
635

ggagtttgcataatgcac ttctctttat aatacacttc tcttttagacc tgtagtgaag 2035

ccgatgcacc attacagtgt atatggagc cagtcttagtc tcaaaaagtt tgtaaatgtt 2095

attctatgtat atactcttta gaccaaaaagc tagatgcccc tgaaaaagcaa gtgttttaga 2155

attgcttctg gatttgccta aattttctcc atgattcttt agaaatgttg catccccaaa 2215  
cttcactgcc atataagata acgggagtga caaggatttt aaagaggatt ttttttatg 2275  
tcccgcatca caaggttgt cgatttacag ttgtttcaa gactgaagta ggatttccac 2335  
cctccattaa tcctcttctc gatgttatacg tttcacttga gcttgtgatg gaagtcaatt 2395  
cctagatatt tataagaaaa aaaaaaaaaa aaaa 2429

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<211> 637  
<212> PRT  
<213> *Abies grandis*

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Leu Lys Ser Leu Ile Ser Ser Asn Val Gln Lys Ala Leu Cys Ile  
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Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu  
35 40 45  
  
Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly  
50 55 60  
  
Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp  
65 70 75 80  
  
Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser  
85 90 95  
  
Tyr Ser Glu Arg Ala Val Thr Val Val Glu Glu Val Lys Glu Met Phe  
100 105 110  
  
Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu  
115 120 125  
  
Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp  
130 135 140  
  
Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser  
145 150 155 160  
  
Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe  
165 170 175  
  
Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His  
180 185 190  
  
Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Gln Lys  
195 200 205  
  
Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg  
210 215 220  
  
Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu

225                    230                    235                    240  
Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Glu  
245                    250                    255  
Val Leu Gln Lys Ile Pro Val Ser Ser Phe Ser Arg Glu Ile Glu Tyr  
260                    265                    270  
Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg  
275                    280                    285  
Asn Tyr Ile Asp Val Tyr Gly Gln Asp Ser Tyr Glu Ser Ser Asn Glu  
290                    295                    300  
Met Pro Tyr Val Asn Thr Gln Lys Leu Leu Lys Leu Ala Lys Leu Glu  
305                    310                    315                    320  
Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr Ile Ser  
325                    330                    335  
Arg Trp Trp Lys Asp Ser Cys Ser Ser His Leu Thr Phe Thr Arg His  
340                    345                    350  
Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Glu Pro  
355                    360                    365  
Lys His Ser Ala Phe Arg Leu Gly Phe Val Lys Thr Cys His Leu Leu  
370                    375                    380  
Thr Val Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Leu Asp Glu Leu  
385                    390                    395                    400  
Gln Leu Phe Thr Thr Ala Phe Lys Arg Trp Asp Leu Ser Glu Thr Lys  
405                    410                    415  
Cys Leu Pro Glu Tyr Met Lys Ala Val Tyr Met Asp Leu Tyr Gln Cys  
420                    425                    430  
Leu Asn Glu Leu Ala Gln Glu Ala Glu Lys Thr Gln Gly Arg Asp Thr  
435                    440                    445  
Leu Asn Tyr Ile Arg Asn Ala Tyr Glu Ser His Phe Asp Ser Phe Met  
450                    455                    460  
His Glu Ala Lys Trp Ile Ser Ser Gly Tyr Leu Pro Thr Phe Glu Glu  
465                    470                    475                    480  
Tyr Leu Lys Asn Gly Lys Val Ser Ser Gly Ser Arg Thr Ala Thr Leu  
485                    490                    495  
Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asn Tyr Ile Leu Gln  
500                    505                    510  
Glu Ile Asp Tyr Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser Leu Leu  
515                    520                    525  
Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly  
530                    535                    540  
Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser  
545                    550                    555                    560

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala  
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro  
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His  
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys  
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu  
625 630 635

<210> 70

<211> 696

<212> DNA

<213> Abies grandis

<400> 70

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cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatatgaaa 180

gaagctgagt gatatctccag tggttatctg ccaacgtttg aggagtacat ggagaccagc 240

aaagtttagtt ttggttatcg catattcgca ttgcaaccca tcctcactat gatatgttccc 300

cttactcacc acatcctgca gaaaatagac tttccattga gtttaatga cttaatatgt 360

tccatccttc gactaaaaaa tgacactcgc tgctacaagg cggacaggc ccgtggagaa 420

gaagcttcgt gatatctgt ttatatgaaa gagaatcctg gatcaacaga ggaagatgct 480

atcaatcata tcaacgctat ggtcaataac ttaatcaaag aagtgaattt ggagcttc 540

cgacaggacg gcaccgctca tattgcttgc aagaaacacg ctttgacat cctcaaagg 600

tcccttcacg gctacaaaata ccgagatggg ttcagcggtt ccaacaagga aaccaagaat 660

tgggtgagga gaacagtctt tgagtctgtt cctttg 696

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<220>

<221> misc\_feature

<222> (1)..(20)

<223> Reverse RACE primer 10-2

<400> 71  
acgaagcttc ttctccacgg 20

<210> 72  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> Reverse RACE primer 10-4

<400> 72  
ggatcccatc tcttaactgc 20

<210> 73  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(27)  
<223> PCR primer AP1

<400> 73  
ccatcctaat acgactcact atagggc 27

<210> 74  
<211> 23  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
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<222> (1)..(23)  
<223> PCR primer AP2

<400> 74  
actcactata gggctcgagc ggc 23

<210> 75  
<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223> PCR primer AG9F

<400> 75  
atggctcttg tttctatctt gccc 24

<210> 76  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223> PCR primer AG9R

<400> 76  
ttacaaaggc acagactcaa ggac 24

<210> 77  
<211> 1890  
<212> DNA  
<213> Abies grandis

<220>  
<221> CDS  
<222> (1)..(1890)

<400> 77  
atg gct ctt gtt tct atc ttg ccc ttg tct tcc aaa tcg gtc ctg cac 48  
Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His  
1 5 10 15

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca 96  
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr  
20 25 30

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc 144  
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser  
35 40 45

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa 192  
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln  
50 55 60

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata 240

Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile			
65	70	75	80
caa tct cta tca acg cct tat ggg gca cct tca tac cgt gaa cgt gct			288
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala			
85	90	95	
gat aga ctt att gtg gaa gta aag ggt ata ttc act tca att tca gcg			336
Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala			
100	105	110	
gaa gat gga gaa cta atc act ccc ctc aat gat ctc att caa cgc ctt			384
Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu			
115	120	125	
tta atg gtc gat aac gtt gaa cgt tta ggg att gat aga cat ttc aaa			432
Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys			
130	135	140	
aat gag ata aaa gca gca cta gac tat gtt tac agt tat tgg aac gaa			480
Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu			
145	150	155	160
aaa ggc att ggc agt gga agt gat agt ggt gtt gct gat ctc aac tca			528
Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser			
165	170	175	
act gcc ctg ggg ttt cga att ctt cga cta cac gga tac agt gtt tct			576
Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser			
180	185	190	
tca gat gtg ttg gaa cac ttc aaa gag gag aag gag aag ggg cag ttt			624
Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe			
195	200	205	
gta tgt tcg gcc atc caa aca gag gaa gag ata aaa agc gtt ctg aat			672
Val Cys Ser Ala Ile Gln Thr Glu Glu Ile Lys Ser Val Leu Asn			
210	215	220	
tta ttt cgg gcc tcc ctc att gcc ttt cct ggg gag aaa gtt atg gaa			720
Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu			
225	230	235	240
gag gct gaa atc ttc tct aaa ata tat tta aaa gaa gcc tta caa aat			768
Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn			
245	250	255	
att gct gtc tcc agt ctt tca cga gag ata gag tac gtt ctg gag gat			816
Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp			
260	265	270	
ggt tgg caa aca aat atg cca aga ttg gaa aca agg aac tac atc gat			864
Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp			
275	280	285	
gta ttg gga gag aac gat cgt gat gag acg tta tat atg aac atg gag			912
Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu			
290	295	300	
aaa ctt tta gaa att gca aaa ttg gag ttc aat att ttt cac tcc tta			960
Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu			

305	310	315	320	
caa cag aga gag cta aaa gac ctc tcc aga tgg tgg aaa gat tcg ggt Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly 325		330	335	1008
ttc tct cac ctg aca ttt tct cgg cat cgt cat gtg gaa ttc tac gct Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala 340	345		350	1056
ctg gca tct tgc att gaa act gat cgc aaa cat tcc gga ttc aga ctc Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu 355	360	365		1104
ggc ttt gcc aaa atg tgt cat ctt atc acg gtt ttg gac gat ata tac Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr 370	375	380		1152
gac acc ttt gga aca atg gag gag ctg gaa ctc ttc act gca gca ttt Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe 385	390	395	400	1200
aag aga tgg gat ccg tct gcc aca gat ttg ctt cca gag tat atg aaa Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys 405	410	415		1248
ggg ttg tac atg gtg gtt tac gaa acc gta aat gaa att gct cga gag Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu 420	425	430		1296
gca gac aag tct caa ggc cga gag acg ctc aac gat gct cga cga gct Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala 435	440	445		1344
tgg gag gcc tat ctt gat tcg tat atg aaa gaa gct gag tgg atc tcc Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser 450	455	460		1392
agt ggt tat ctg cca acg ttt gag gag tac atg gag acc agc aaa gtt Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val 465	470	475	480	1440
agt ttt ggt tat cgc ata ttc gca ttg caa ccc atc ctc act atg gat Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp 485	490	495		1488
gtt ccc ctt act cac cac atc ctg cag gaa ata gac ttt cca ttg agg Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg 500	505	510		1536
ttt aat gac tta ata tgt tcc atc ctt cga ctt aaa aat gac act cgc Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg 515	520	525		1584
tgc tac aag gcg gac agg gcc cgt gga gaa gaa gct tcg tgt ata tcg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser 530	535	540		1632
tgt tat atg aaa gag aat cct gga tca aca gag gaa gat gct atc aat Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn 545	550	555	560	1680

cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag		1728
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu		
565	570	575
ctt ctc cga cag gac ggc acc gct cat att gct tgc aag aaa cac gct		1776
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala		
580	585	590
ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg		1824
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly		
595	600	605
ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc		1872
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val		
610	615	620
ctt gag tct gtg cct ttg		1890
Leu Glu Ser Val Pro Leu		
625	630	

<210> 78  
<211> 630  
<212> PRT  
<213> Abies grandis

<400> 78

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Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr			
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Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser			
35	40	45	
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln			
50	55	60	
Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile			
65	70	75	80
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala			
85	90	95	
Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala			
100	105	110	
Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu			
115	120	125	
Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys			
130	135	140	
Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu			
145	150	155	160
Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser			
165	170	175	

Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser  
180 185 190

Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe  
195 200 205

Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn  
210 215 220

Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu  
225 230 235 240

Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn  
245 250 255

Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp  
260 265 270

Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp  
275 280 285

Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu  
290 295 300

Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu  
305 310 315 320

Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly  
325 330 335

Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala  
340 345 350

Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu  
355 360 365

Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr  
370 375 380

Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe  
385 390 395 400

Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys  
405 410 415

Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu  
420 425 430

Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala  
435 440 445

Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser  
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val  
465 470 475 480

Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp  
485 490 495

Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg

500

505

510

Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg  
515 520 525

Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser  
530 535 540

Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn  
545 550 555 560

His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu  
565 570 575

Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala  
580 585 590

Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly  
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<210> 81  
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<210> 82  
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<400> 82  
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<210> 83  
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<222> (1)..(25)  
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<210> 84  
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<400> 84  
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<210> 85  
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<400> 85  
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<210> 86  
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<220>  
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<210> 87  
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<223> PCR primer 6-BamHI

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cacccatagg ggatccttag ttaatattg

29

<210> 88

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<223> PCR primer 8-NdeI-M

<400> 88

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<400> 89

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<400> 90

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<210> 91

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<400> 91  
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<210> 95  
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<400> 95  
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<210> 96  
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<400> 96  
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<210> 97  
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<400> 97

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<400> 101  
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<400> 102  
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<210> 103  
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<400> 103  
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<210> 104  
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<220>  
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<222> (1)..(25)  
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